

Figure 1
Fatty Acid Biosynthetic Pathway

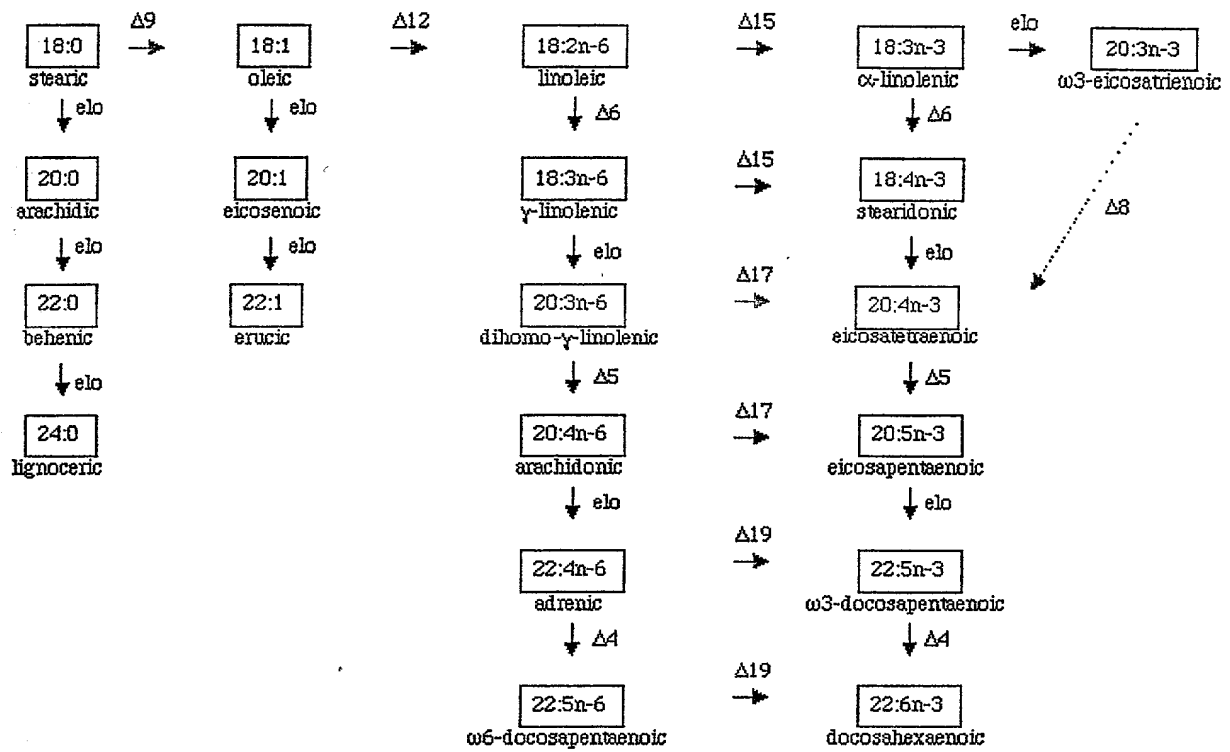


Figure 2

Gene Sequence of Delta 6-Desaturase from *Staphylococcus aureus* (ATCC 56851)

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1  ATGGTCCAGG  GGC AAAAGGC  CGAGAAGATC  TCGTGGGCGA  CCATCCGTGA
51  GCACAACCGC  CAAGACAACG  CGTGGATCGT  SATCCACCAC  AAGGTGTACG
101 ACATCTCGGC  CTTTGAGGAC  CACCCGGGCG  GCGTCGTGAT  GTTCACGACG
151 GCGGGCGAAG  ACGCGACCGA  TGGTTTCGCT  GTCTTCCACC  CGAGCTCGGC
201 GCTCAAGCTC  CTGAGCAGT  ACTACGTCGG  CGACGTCGAC  CAGTCGACGG
251 GGGCCGTCGA  CACGTCGATC  TCGGACGAGG  TCAAGAAAGG  CCAATCGGAC
301 TTCATTGCGT  CGTACCGCAA  GCTGCGCCTT  GAAATCAAGC  GCCTCGGCTT
351 GTACGACTCG  AGCAAGCTCT  ACTACCTCTA  CAAATGCGGC  TCGACGCTGA
401 GCATTGCGCT  TGTGTCGGCG  GCCATTTGCC  TCCACTTTGA  CTCGACGGCC
451 ATGTACATGG  TCGCGGCTGT  CATCCTTGGC  CTCTTTTACC  AGCAATGCGG
501 CTGGCTCGCC  CATGACTTTC  TGCACCACCA  AGTGTTTGAG  AACCCTTGT
551 TTGGCGACCT  CGTCGGGCTC  ATGGTCGGCA  ACCTCTGGCA  GGGCTTCTCG
601 GTGCAATGGT  GGAAGAACAA  GCACAACAGC  CACCATGCGA  TCCCCAAGT
651 CCAAGCGACG  CCGAGATCG  CCTTCCACGG  CGACCCGGAC  ATTGACAGCA
701 TGGCGATTCT  CGGTGGTGG  CTCAAGATGG  CGCAGCAGCG  GGTGCACTCG
751 CCCGTGCGGC  TCTTCTTCAT  GCGCTACCAA  GCGTACCTGT  ACTTTCCTAT
801 CTGCTCTTT  GCGGTATCT  CGTGGGTGAT  CCAATCGGCG  ATGTACGCTT
851 TCTACAACT  TGGGCCCCGG  GGCACCTTGG  ACAAGGTCCA  GTACCCGCTG
901 CTGAGCGCG  CCGGCTCCT  CCTCTACTAC  GGTGGAAGC  TCGGCTTGT
951 GTACGAGGCC  AACATGTCGC  TGCTCCAAGC  GGTGCGTTC  CTCTTTGTTA
1001 GCGAGGCGTC  GTGCGGCTC  TTCTCGCGA  TGGTCTTTAG  CGTCGGCCAC
1051 AACGGCATGG  AGGTCTTTGA  CAAGGACAGC  AAGCCCGATT  TTTGGAAAGT
1101 GCAAGTGCTC  TCGAGCGCGA  ACGTGACGTC  GTCGCTCTGG  ATCGACTGGT
1151 TCATGGGCGG  CCTCAACTAC  CAGATCGACC  ACCACTTGT  CCCGATGGTG
1201 CCCCGCACCA  ACCTCCCGGC  GCTCAACGTG  CTGTCAAAT  CGCTCTGCAA
1251 GCAATACGAC  ATCCCATACC  ACGAGACGGG  CTTCATCGCG  GGCATGGCGG
1301 AGGTGTCGCT  GCACCTCGAG  CGCATCTCGA  TCGAGTTCTT  CAAGGAGTTT
1351 CCCGCCATGT  AA

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Figure 3

Amino Acid Sequence of Delta 6- Desaturase from *Staphylococcus aureus* (ATCC 56851)

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1  MVQSQKAEKI SKATIREHNR QDNAMIVIHK KVVDISAFED HEGGVVME TQ
51  AGEDATDAFA VEHPSALKL LEQYYVG DVD QSTAAVDTSI SDEVKKSQSD
101  FIASVRKLRL EVKREGLYDS SKLYYLYKCA STLSTALVSA AICLHEDSTA
151  MYMYAAVIEG LEYQCCGMHA HDEEMHQVEE NHLEGDLVGV M/GNIMQGIS
201  VQMMIQKQNT HHAIPNIMAT PEIAFHGDDE IDTMPILAMS LKMAQHAYDS
251  PVGLFFMR YQ AYLVE EILIE ARISWVIQSA MYAEYNVGP GTEDEKQYPL
301  LERAGLLLYY GNNIG LVYAA NMSLLQAAAE LEVSQLASGL FLAMYSVGH
351  NGMEYEDKDS KPEFWKIQVL STRNV TSSLM IDWEMGG LNY QIDHHLF RMV
401  ERHNLPAENV LVKSLCKQYD IPEHE TGFIA GMAEVVVHLE RISIEEFKEF
451  PAM*
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Figure 4

Gene Sequence of Delta 5- Desaturase from *Styromonas danica* (ATCC 56851)

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1  ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
51  GCCGGTGGCC GGCAGAAGGG CCTTTACATG GCAGGAGGTC GCGCAGCACA
101 ACACGGCGGG CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
151 ACCGAGTGGG CCAACAAGCA CCCCGCGGGC GCGGAGATGG TGCTGCTGCA
201 CGCGGCTCGC GAGGCCACCG ACACGTTCSA CTCGTACCAC CCGTTCAGCG
251 ACAAGGCCGA GTCGATCTTG AACAAATATG AGATTGGCAC GTTCAGGGG
301 CGGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
351 CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
401 ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTGCGCGGC
451 CTCGCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
501 GGGCGCGGGC CTCTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
551 TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCATTAC
601 GTCGTGCGCC GCTTTGCCAT GGAATGGTTT GCGGCGGGCT CGATGGTGTG
651 ATGGCTCAAC CAGCAGTGG TGGGCCACCA CATCTACAG AACGTGCGGG
701 GCTCGGACCC GGAATCTTCG GTCAACATGG ACGGGGACAT CCGCGCGATC
751 GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT
801 TCCGCCGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA
851 CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
901 GCGCTCTCSA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGGCCTT
951 CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001 ACCTTGCGAT CTTCTTCTTC GCGGAGTTTG TCACGGGCTG GTACCTCGCG
1051 TTCAACTTCC AAGTAAGCCA TGCTCGACC GAGTGGGGCT ACCCATGCGG
1101 CGACGAGGCC AAGATGGGCG TCCAGGACGA GTGGGCASTC TCGCAGGTCA
1151 AGACGTGCGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGGC
1201 GGGCGCTCA ACTACAGGT CGTGACCCAC TTGTTCCTCA GCGTGTGCGA
1251 GTACCACTAC CCGGCGATCG CGCCCATCAT GGTGACGTC TGCAAGGAGT
1301 ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGGC
1351 CACTTGAAAG ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
1401 CCACATGGGC TAA

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Figure 5

Amino Acid Sequence of Delta 5- Desaturase from *Styruibacterium diuturnum* (ATCC 56851)

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1   MAPQTEIRQR HAAVAETPYA GKKEFTMCEY AQHNTAASAM IIRGKYVDY
51  TEWANKHPGG REMVLHAGR EATDTFDSYH EFSDKAESIL NKYEIGTF TG
101 PSEFPTFKED TGEYKECRKR VGEYFKKNNL HPQDGF PGLW RMMVVEAVAG
151 LALVGMHFT IFALQLAAAA LFGVCQALPL LHVMDSSHA SYTNMPEFHY
201 VVGRFAMDWE AGGSMVSWLN QHVVGHHIYT NVAGSDPDLF VMDGDIRRI
251 VNRQVFQPMY AFQHIYLPPL YGVLSIKERI QDETDTEGSH TNGPIRYNPH
301 ALSTMAMIS SKSEWAFYRY YLLPLAVLQMP IKTYLAIEFL AEFVTGMVLA
351 ENFQVSHVST ECGYPCGDEA KMAIQDE MAY SQVKTSDVYA HGSMTTEFLA
401 GADNQQVYHH LFPSVSYHYH PAIARITVDV CKEYNIKYAI LEDETAAFVA
451 HKKHLRMMGQ QGLAATIHMG *

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Figure 6

Gene Sequence of Delta 5- Desaturase from *Thermodictyon aurum* (ATCC 34304)

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1  ATGGGACGCG GCGGCGAAGG TCAGGTGAAC AGCGCGCAGG TGGCACAAGG
51  CCGTSCGGGA ACSCGAAAGA CGATCCTGAT CGAGGCGGAG GTCTACGATG
101  TCAOCAAATT TAGGCACCCC GCGGCGTCGA TCATCAAGTT TCTACGACC
151  GACGSCACCG AGGCTGTGGA CGGACGAAAC GCGTTTCGCG AGTTTCACTG
201  CCGTSCGGGC AAGGCGGAAA AGTACCTCAA GAGCCTGCCC AAGTCTGCGG
251  CGCAGAGCAA GATGAAGTTT GAGGCCAAGG AGCAGGCCCC GCGGACGCGG
301  ATCAGCGCAG ACTACGTCAA GCTGCGCGAG GAGATGGTGG CCGAGGGCCT
351  CTTCAAGCCC GCGCCCCCTC ACATTGTCTA CAGGTTTGGG GAGATCGCAG
401  CCTGTTCGCG GCGCTCGTTC TACCTGTTTT CGATGCGCGG AAACGTGTTT
451  GCCACGCTCG CGGCCATCGC AGTCGGGGGG ATCGCGCAGG GCGGCTGCGG
501  CTGGCTCATG CAAGAGTGCG GACACTTCTC GATGACCGGG TACATCCCGC
551  TTGACGTGCG CCTGAGGAG CTGGTGTACG GCGTGGGGTG CTGATGTGCG
601  GCGAGCTGGT GCGCGTTCA GCACAACAAG CACCACGCGA CCGCGCAGAA
651  ACTCAAGCAC GAGTTCGACC TCGACACCCCT GCGGCTGCTT GCGTTCAACG
701  AGAAGATGCG CGCAGAGGTG CGCCCGGGCT CGTTCAGGGC CAAGTGGCTC
751  TCGGCGCAGG CGTACATTTT TGCGCGGGTG TCGTGGCTTC TGGTTGGTCT
801  CTTCTGGACC CTGTTTCTGC ACCCGCGCCA CATGCGCGCG ACAGGCCACT
851  TTGCTGAGAT GCGCGCGCTC GCGGTGCGCG TCGTGGGCTG GCGCGCGCTC
901  ATGCACTCGT TCGGGTACAG CGGAGCGGAC TCGTTCGGTC TCTACATGGC
951  CACCTTTGGC TTTGGCTGCA CCTACATCTT CACCAACTTT GCGGTCAGCC
1001  ACAAGCACTT CGAGCTCACC GAGCCGGAGG AGTTCCTGCA CTGGGTGAGG
1051  TACGCGCGCG TGCACGAGC CAACGTGTCC AACGACTCGT GGTTCATCAC
1101  CTGGTGGATG TCGTACCTCA ACTTTGAGAT CGAGCACCAC CTCTTTCCGT
1151  CGCTGCCCCA GCTCAACGCG CCGCGCGTGG CCGCGCGCGT CCGCGCGCTC
1201  TTCGAGAACG ACAGCATGGC TTACGACGAG CGCCCGTACC TTACCGCGCT
1251  TGGGACACAG TTTGCCAACC TGACGCGCTT GGGCCAAAC GCGGCGCAGG
1301  GCGGCGCAA GCGCGCTTAG

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Figure 7

Amino Acid Sequence of Delta 5- Desaturase from *Thermotrichium aurum* (ATCC 34304)

1 MRRGEGQVW SAQVAGGAG TRKTILLIGE VYDVTNERHP GGSIIKE LTT
51 DGTEAYDATN AFRFEHCRSG KAEKYLKSLP KLGAPSKMCF DAKEDARRDA
101 ITRDYVKLRE EMVAEG LEKP APDHTVYREA EIAALEFAASE YLESMRGNYE
151 ATLAATAVGG IAGRCGNIM HECGHE SMTG YIBEDVRLQE LVYGVGC SMS
201 ASMRYVQHNK HHATEQKLNH DVLDLTLEIV AENEKIDAKV RRGSEQAKML
251 SAQAYIFAPV SCFLVG LEKT LEIMERHMER TSHFAEMAY AVRYVGMAL
301 MHSEGVSGSD SEGLYMATFG FGCTYIE TNE AVSHTHEDVT EDEE LHWVE
351 YALHTTNYV NDSWEITNM SYLNFQIEHM LEPSLEQLNA PRVAPRVRL
401 EEKKGMAIDE RPYLTALGDT EANLHAYGQN AGQAAAKAA

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Figure 8

1 GAATTCACCA TGGGTGCGG AGCAGAGGA GAGCCAAGG AGGCCACAGA
 51 GCTGAAGAGC AGCCCAAGTG AGCAGGTAA GGTGTTGCTC ATTACGGGC
 101 AGCTGTACGA TGCACCAAC TTCAGGCATC CTGGTGGCTC CATCATCAA
 151 TATTTGTGCA CCGATGGCAA GGAGTAGTT GATGCAACCG AAGCGTACAA
 201 GGAGTTCCAC TGCAGATCCT CGAAGCGGT CAAGTACCTC AACTCCCTGC
 251 CAAAGATCGA CGGCCCAATC AAGTACAAAT ACGACGCAA GGAGCAGGT
 301 CGCCATGACA AACTCACGAG GGAGTATGTA GCTCTCCGG AACAGTCTGT
 351 CAAGAGGGA TACTTTGACC CCAGCCCGCT CCACATTATC TACAGATGCG
 401 CCGAGTTGGC AGCCATGTTT GCTCTCTCGT TCTACCTTTT CTCCTTCAAG
 451 GGTAACGTCA TGGCCACTAT TGCTGCCATC GTGATGGGG GTGCGGTGCA
 501 GGTGCTTGT GGTGGCTCA TGCATGAAG TGGCCACTAC AGCATGACCG
 551 GAAACATCCC TGTGACTTG CGCCTTCAAG AGTTTTTGA CGGAATTGGG
 601 TGTGGCATGA GCGGGCTTG GTGGAGAAGC CAGCACACA AGCACACGC
 651 CACCCCCCAA AAGCTCAAGC ATGACGTTGA TTTGGACACT CTTCCTCTTG
 701 TCGCTGGAA CGAGAAAATT GCCCGTCGCG TCAAGCCAGG TAGCTTCCAG
 751 GCAAAGTGGC TTCACTCTCA GGGATACATC TTTGCCCCAG TCTCCTGCCT
 801 TCTCGTTGGT CTCCTCTGGA CTTTGTACTT GCATCCTCGC CACATGATCC
 851 GCACCAAGCG CACTTCGAG ATATTTTCTG TCGCTCTGCG CTACGTATGC
 901 TGGTCTCGC TTTCTTTGAG CATGGGCTAC ACTGTGGAG AGTCTCTGGG
 951 TCTCTATGTG CTTACTTTTG GACTTGGCTG TACCTACATC TTTACGCATT
 1001 TTGCTGTAAG CCACACCCAC TTGCCAGTGT CCGAGGAGGA CGAGTACCTG
 1051 CACTGGGTG AGTACGCTG GCTGCACACC ACGAACGTTG CCATCGACTC
 1101 GTACGTTGTC ACCTGGCTGA TGAGCTACCT CAACTTTCAG ATCGAGCACC
 1151 ACTTGTCCC TTGCTGCCCG CAGTTCCGCC ACCCTGCAAT CTCCTCTGCG
 1201 GTCAAGAAAC TTTTCGAGGA CAATGGTCTG GTATACGACG CCGGTCTATA
 1251 CGTCCAGGCG CTCAAGGATA CCTTCGGCAA CCTACACGAA GTGGGCGTCA
 1301 ACGCTGGCCA AGCTGCCAAG AGCGAGTAAG ATCTCGAG

Start/stop underlined

Figure 9

1 MGRGAQGEPR QATELKSSPS EQRKVLIDG QLYDATNFRH PGGSIKYL
51 TDGKEVV DAT EAYKEFHCRS SKAVKYLNSL PKIDGPIKYK YDAKEQARHD
101 KLREYVALR EQLVKEGYFD PSLHIYRC AELAAMFALS FYLFSEKGNV
151 MATIAAIVIG GCVQGRGWL MHEAGHYSMT GNIPVDLRLQ EFLYGIGCGM
201 SGAWWRSQHN KKHATPQKIK HDVDLDTLPL VAMNEKIARR VKPGSFQAKW
251 LHLOGYIFAP VSCLLVGLFW TLYLHPRHMI RTRNFEIFS VALRYVCWFS
301 LLLSMGYTVG ESLGLYVLTFF GLGCTYIFTH FAVSHTHLPV SEDEYVHWW
351 EYAALHTTNV AIDSYYVTWL MSYLNFIQIEH HLFPCCPQFR HPAISSRVKK
401 LFEDNGLVYD ARSYVQALKD TFGNLHEVGV NAGQAAKSE

Figure 10

1 CCATGGGCGG CGGCGGCGAG AAAAGCGAGG TGGACCAGGT GCAGCCACAA
 51 AAGACCGAGC AGCTCCAGAA GGCCAAAGTG GAGATGTTG TTCCGATCAA
 101 TGGAGTCGAA TACGACGTCA CGGACTATCT CAGAAAAACAC CCTGGTGGCA
 151 GCGTGATCAA GTACGGGCTT GCCAACACCG GCGCTGATGC CACGTCCCTC
 201 TTTGAAGCGT TCCACATGCG CTCAAAGAAG GCTCAGATGG TGCTCAAGTC
 251 TCTCCCAAAG CGTGTCCGG TCCTCGAGAT CCAGCCAAAC CAGCTTCCAG
 301 AGGAGCAGAC CAAGGAGCG GAGATGCTGC GTGATTTAA AAAATTGAG
 351 GATGAGATTC GCCGGGATGG ATTGATGGAA CCTTCCCTCT GGCATCGCGC
 401 TTACAGATTA TCAGAGCTTG TAGGTATGTT CACGCTCGGC CTCTACCTCT
 451 TCTCGTTAAA CACTCCTCTG TCTATTGCTG CTGGTGTCT CGTCCACGGT
 501 CTCTTTGGTG CATCTGTGG ATGGTGCCAG CATGAGGCGC GCCACGGCTC
 551 CTTTTTTTAC AGCCTTTGGT GGGCAAGCG TGTACAGGCC ATGTTGATCG
 601 GGTTCGTCT AGGAACATCC GGCACATGT GGAACATGAT GCACAACAAG
 651 CATCATGCTG CCACCCAAA GGTTCATCAC GACCTTGACA TTGACACAAC
 701 TCCTTTTGTA GCTTCTTCA AACTGCAAT TGAGAAAAAC AGATGGAAGG
 751 GCTTTTCCAA GGCTTGGGTG CGCTTTCAGG CTTTCACGTT CATTCCTGTC
 801 ACCAGCGGCA TGATCGTCAT GCTGTCTTGG CTGTTTTTTC TCCACCTCTG
 851 CCGCGTCGTT CAAAAGAAGA ACTTTGAGGA GGGTTTTTGG ATGCTGTCTGA
 901 GCCACATTGT GCGCACCTAT CTCCTCCACC TTGTGACCGG CTGGGAGAGC
 951 CTCGCTGCAAT GCTACCTTGT TGGGTATTGG GCGTGCATGT GGGTGTCCGG
 1001 TATGTATTG TTTGGCCACT TTTGCTCTC CCACACTCAT ATGGACATTG
 1051 TGGAGGCGGA CGTGCATAAG AACTGGGTCA GGTACGCTGT TGACCACT
 1101 GTTGACATCA GCCCATCCAA CCCGCTCGTG TGCTGGGTCA TGGGTTACCT
 1151 CAACATGCAG ACCATCCACC ACTTGTGGCC TGCCATGCC CAGTACCACC
 1201 AGGTCGAGGT CTCACGCCGC TTTGCCATCT TCGCCAAAA ACACGGCCTC
 1251 AACTACCGCG TCGTCTCTTA CTTTGAGGCT TGGCGCCTGA TGCTCCAAAA
 1301 TCTTGTGAC GTGGTTCCC ACTACCATGA GAACGGTGTG AAGCGGCCCC
 1351 CAAAGAAAGC CAAGGCGCAG TAGAAAGCTA T

start/stop underlined

Figure 11

1 MGRGGEKSEV DQVQPKTEQ LQKAKWEDVV RINGVEYDVT DYLRKHPGGS
51 VIKYGLANTG ADATSLFEAF HMRSKKAQNV LKSLPKRAPV LEIQPNQLPE
101 EQTKEAEMLR DKKFEDEIR RDGLMEPSEW HRAYRLSELV GMFTLGLYLF
151 SLNTELSIAA GVLVHGLFGA FCGWCQHEAG HGSEFFYSLWW GKRVOAMLIG
201 FGLGTSGDMW NMMHNKHHAA TQKVHHDLDI DTTPEFAFFN TAFEKNRWKG
251 FSKAWVRFOA FTFIPVTSGM IVMLFWLFFL HP RRVVQKKN FEEGFWMLSS
301 HIVRTYLFHL VTGWESLAAC YLVGYWACMW VSGMYLFGHF SLSTHMDIV
351 EADVHKNWVR YAVDHTVDIS PSNPLVCWMV GYLNMQTIHH LWPAMPQYHQ
401 VEVSRRAIF AKKHGLNYRV VSYFEAWRLM LQNLADVGSH YHENGVKRAP
451 KKAKAQ

Figure 12

pRAT-2a	1	MGRGAQGEPRQATELKSSPSEQRKVLLIDGQLYDATNFRHPGGSI	45
pRAT-2c	1	MGRGAQGEPRQATELKSSPSEQRKVLLIDGQLYDATNFRHPGGSI	45
pRAT-2a	46	IKYLC TDGKEVVDAT EAYKEFFHCRSSKADKY LNSLPKIDGPIKYK	90
pRAT-2c	46	IKYLC TDGKEVVDAT EAYKEFFHCRSSKADKY LNSLPKIDGPIKYK	90
pRAT-2a	91	YDAKEQARHDKL TREYVALREQLVKEGYFDPSPLHIIYRCAELAA	135
pRAT-2c	91	YDAKEQARHDKL TREYVALREQLVKEGYFDPSPLHIIYRCAELAA	135
pRAT-2a	136	MFALSFY LFSFKGNVVA TIAAIVIGGC VQGRCGWLMHEAGHY SMT	180
pRAT-2c	136	MFALSFY LFSFKGNVVA TIAAIVIGGC VQGRCGWLMHEAGHY SMT	180
pRAT-2a	181	GNIPVDLRLQEF LYGIGCGMSGAWWR RQHKNHHA TPQK LKHDVDL	225
pRAT-2c	181	GNIPVDLRLQEF LYGIGCGMSGAWWR RQHKNHHA TPQK LKHDVDL	225
pRAT-2a	226	DTLPLVAWNEK IARRVKPGSFQAKW IHLQGY IFAPVSC LLLVGLFW	270
pRAT-2c	226	DTLPLVAWNEK IARRVKPGSFQAKW IHLQGY IFAPVSC LLLVGLFW	270
pRAT-2a	271	TLYLHPRHM IRTKRNFEI FSV ALRYVCWFSL LLSMGY TVGESLGL	315
pRAT-2c	271	TLYLHPRHM IRTKRNFEI FSV ALRYVCWFSL LLSMGY TVGESLGL	315
pRAT-2a	316	YVLT FGLGCTY IFTHF AVSH THLPVSEED EY LHWVEY AALHTTNV	360
pRAT-2c	316	YVLT FGLGCTY IFTHF AVSH THLPVSEED EY LHWVEY AALHTTNV	360
pRAT-2a	361	AIDSYVVTWLM SYLNFQIEHHLFPCCPQFRHPA ISSRVKKLFEDN	405
pRAT-2c	361	AIDSYVVTWLM SYLNFQIEHHLFPCCPQFRHPA ISSRVKKLFEDN	405
pRAT-2a	406	GLVYDARSYVQA LKDTFGNLHEVGVNAGQA AKSE	439
pRAT-2c	406	GLVYDARSYVQA LKDTFGNLHEVGVNAGQA AKSE	439

Figure 13

pRAT-1a	1	MGRGGEKSEVDQVQPPQKTEQLQKAKWEDVVRINGVEYDVTDYLR	44
pRAT-1b	1	MGRGGEKSEVDQVQPPQKTEQLQKAKWEDVVRINGVEYDVTDYLR	44
pRAT-1a	45	KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMV LKSLPKRA	88
pRAT-1b	45	KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMV LKSLPKRA	88
pRAT-1a	89	PVLEIQPNQLPEEQTKAEMLRDFKKFEDEIRRDGLMEPSFWHR	132
pRAT-1b	89	PVLEIQPNQLPEEQTKAEMLRDFKKFEDEIRRDGLMEPSFWHR	132
pRAT-1a	133	AYRLSELVGMFTLGLYLFSLNTPLSIAAGVLVHGLFGAFCGWCQ	176
pRAT-1b	133	AYRLSELVGMFTLGLYLFSLNTPLSIAAGVLVHGLFGAFCGWCQ	176
pRAT-1a	177	HEAGHGSEFFYSLWWGKRVQAMLIGFGLGTSGDMWNMMHNKHHAA	220
pRAT-1b	177	HEAGHGSEFFYSLWWGKRVQAMLIGFGLGTSGDMWNMMHNKHHAA	220
pRAT-1a	221	TQKVHHDDLIDITTPFVAFFNTAFENRWKGFSAWVRFQAFTFI	264
pRAT-1b	221	TQKVHHDDLIDITTPFVAFFNTAFENRWKGFSAWVRFQAFTFI	264
pRAT-1a	265	PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWM LSSHIVRTYLF	308
pRAT-1b	265	PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWM LSSHIVRTYLF	308
pRAT-1a	309	HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA	352
pRAT-1b	309	HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA	352
pRAT-1a	353	DVHKNWVRYAVDHTTVDISPSNPLVCWVMGYLNMQTIIHHLWPAMP	396
pRAT-1b	353	DVHKNWVRYAVDHTTVDISPSNPLVCWVMGYLNMQTIIHHLWPAMP	396
pRAT-1a	397	QYHQVEVSRRFAIFAKKHGLNRYRVVSYFEAWRLMLQN LADVGS	440
pRAT-1b	397	QYHQVEVSRRFAIFAKKHGLNRYRVVSYFEAWRLMLQN LADVGS	440
pRAT-1a	441	YHENGVKRAPKKAKAQ	456
pRAT-1b	441	YHENGVKRAPKKAKAQ	456

Figure 14

1 ATGGTGGCAG GCAAATCAGG CGCTGCGGCG CACGTGACTC ACAGCTCGAC
51 ATTGCCCCGT GAGTACCATG GCGCGACCAA CGACTCGCGC TCTGAGGCGG
101 CCGACGTCAC CGTCTCTAGC ATCGATGCTG AAAAGGAGAT GATCATCAAC
151 GGCCGCGTGT ATGACGTGTC GTCATTTGTG AAGCGGCACC CAGGTGGCTC
201 GGTGATCAAG TTCCAGCTGG GCGCCGACGC GAGCGACGCG TACAACAAC
251 TTCACGTCCG CTCCAAGAAG GCGGACAAGA TGCTGTATTC GCTCCCGTCC
301 CGGCCGGCCG AGGCCGGCTA CGCCCAGGAC GACATCTCCC GCGACTTTGA
351 GAAGCTGCGC CTCGAGCTGA AGGAGGAGGG CTACTTCGAG CCCAACCTGG
401 TGCACGTGAG CTACAGGTGT GTGGAGGTTC TTGCCATGTA CTGGGCTGGC
451 GTCCAGCTCA TCTGGTCCGG GTACTGGTTC CTCGGCGCGA TCGTGGCCGG
501 CATTGCGCAG GGCCGCTGCG GCTGGCTCCA GCATGAGGGT GGGCACTACT
551 CGCTCACCGG CAACATCAAG ATCGACCGGC ATCTGCAGAT GGCCATCTAT
601 GGGCTTGGCT GCGGCATGTC GGGCTGCTAC TGGCGCAACC AGCACAAACA
651 GCACCACGCC ACGCCGCAGA AGCTCGGGAC CGACCCCGAC CTGCAGACGA
701 TGCCGCTGGT GGCCTTCCAC AAGATCGTCG GCGCCAAGGC GCGAGGCAAG
751 GGCAAGGCGT GGCTGGCGTG GCAGGCGCCG CTCTTCTTTG GCGGGATCAT
801 CTGCTCGCTC GTCTCTTTTC GCTGGCAGTT CGTGCTCCAC CCCAACCACG
851 CGCTGCGCGT GCACAATCAC CTGGAGCTCG CGTACATGGG CCTGCGGTAC
901 GTGCTGTGGC ACCTGGCCTT TGGCCACCTC GGGCTGCTGA GCTCGCTCCG
951 CCTGTACGCC TTTTACGTGG CCGTGGGCGG CACCTACATC TTCACCAACT
1001 TCGCCGTCTC GCACACCCAC AAGGACGTCG TCCCGCCCAC CAAGCACATC
1051 TCGTGGGCAC TCTACTCGGC CAACCACAG ACCCACTGCT CCGACTCGCC
1101 CTTTGTCAAC TGGTGGATGG CCTACCTCAA CTTCCAGATC GAGCACCACC
1151 TCTTCCCGTC GATGCCGCAG TACAACCACC CCAAGATCGC CCCGCGGGTG
1201 CGCGCGCTCT TCGAGAAGCA CGGGGTCGAG TATGACGTCC GGCCATACCT
1251 GGAGTGTTTT CGGGTCACGT ACGTCAACCT GCTCGCCGTA GGCAACCCGG
1301 AGCACTCCTA CCACGAGCAC ACGCACTAG

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Figure 15

1 MVAGKSGAAA HVTHSSTLPR EYHGATNDSR SEAADVTVSS IDAEKEMIIN
51 GRVYDVSSFV KRHPGGSVIK FQLGADASDA YNNFHVRSKK ADKMLYSLPS
101 RPAEAGYAQD DISRDFEKLRL LELKEEGYFE PNLVHVSYRC VEVLAMYWAG
151 VQLIWSGYWF LGAIVAGIAQ GRCGWLQHEG GHYSLTGNIK IDRHLQMAIY
201 GLGCGMSGCY WRNQHNKHHA TPQKLGTDPD LQTMPLVAFH KIVGAKARGK
251 GKAWLAWQAP LFFGGIICSL VSFGWQFVLH PNHALRVHNN LELAYMGLRY
301 VLWHLAFGHL GLLSSLRLYA FYVAVGGTYI FTNFAVSHTH KDVVPPTKHI
351 SWALYSANHT TNCSDSPFVN WWMAYLNFQI EHHLFPSMPQ YNHPKIAPRV
401 RALFEKHGVE YDVRPYLECF RVTYVNLLAV GNPEHSYHEH TH

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